

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECH
SYSTEMS
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MAR 08 2002

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/479,608A

Source: 1600

Date Processed by STIC: 12/6/01

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DEC 28 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTIONSERIAL NUMBER: 091479,608A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☒ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☒ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/479,608A

DATE: 12/06/2001

TIME: 16:31:21

Input Set : A:\35918.txt

Output Set: N:\CRF3\12062001\I479608A.raw

Does Not Comply
Corrected Diskette Needed

5 <110> APPLICANT: Drmanac, R.
6 Drmanac, S.
7 Kita, D.
8 Cooke, C.
9 Xu, C.
11 <120> TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
13 <130> FILE REFERENCE: 30311/35918
15 <140> CURRENT APPLICATION NUMBER: US 09/479,608A
16 <141> CURRENT FILING DATE: 2000-01-06
18 <150> PRIOR APPLICATION NUMBER: US 60/115,284
19 <151> PRIOR FILING DATE: 1999-01-06
21 <160> NUMBER OF SEQ ID NOS: 71
23 <170> SOFTWARE: PatentIn version 3.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 10
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Hypothetical sequence
33 <400> SEQUENCE: 1
34 aaaaaaaaaa
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 10
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: Hypothetical sequence
45 <400> SEQUENCE: 2
46 acacacacac
48 <210> SEQ ID NO: 3
49 <211> LENGTH: 20
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION: Hypothetical sequence
56 <400> SEQUENCE: 3
57 atctgtgtct gaagtagtcc
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 20
61 <212> TYPE: DNA
62 <213> ORGANISM: Artificial Sequence
64 <220> FEATURE:
65 <223> OTHER INFORMATION: Hypothetical sequence
67 <400> SEQUENCE: 4
68 atctctggct gaagtagtcc
70 <210> SEQ ID NO: 5
71 <211> LENGTH: 43

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

- invalid response, please explain source
See error summary sheet, item 11

10

10

20

20

Input Set : A:\35918.txt
Output Set: N:\CRF3\12062001\I479608A.raw

72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: Hypothetical sequence
78 <220> FEATURE:
79 <221> NAME/KEY: misc_feature
80 <222> LOCATION:
81 <223> OTHER INFORMATION: b = C or G or T
83 <400> SEQUENCE: 5
84 bbbbbbattt chbbbbgcac tbbbbgtttg bbbacacgbb bbb 43
86 <210> SEQ ID NO: 6
87 <211> LENGTH: 43
88 <212> TYPE: DNA
89 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: Hypothetical sequence
94 <220> FEATURE:
95 <221> NAME/KEY: misc_feature
96 <222> LOCATION:
97 <223> OTHER INFORMATION: b = C or G or T
99 <400> SEQUENCE: 6
100 bbbbbbattt gbbbacactb bbbgtttchb bbbgcacgbb bbb 43
102 <210> SEQ ID NO: 7
103 <211> LENGTH: 10
104 <212> TYPE: DNA
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: Hypothetical sequence
110 <400> SEQUENCE: 7
111 ggtctcccca 10
113 <210> SEQ ID NO: 8
114 <211> LENGTH: 10
115 <212> TYPE: DNA
116 <213> ORGANISM: Artificial Sequence
118 <220> FEATURE:
119 <223> OTHER INFORMATION: Hypothetical sequence
121 <400> SEQUENCE: 8
122 gtctcccca 10
124 <210> SEQ ID NO: 9
125 <211> LENGTH: 10
126 <212> TYPE: DNA
127 <213> ORGANISM: Artificial Sequence
130 <220> FEATURE:
131 <223> OTHER INFORMATION: Hypothetical sequence
133 <400> SEQUENCE: 9
134 tctccccaag 10
136 <210> SEQ ID NO: 10
137 <211> LENGTH: 10
138 <212> TYPE: DNA

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139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Hypothetical sequence
144 <400> SEQUENCE: 10
145 ctccccaagg 10
147 <210> SEQ ID NO: 11
148 <211> LENGTH: 10
149 <212> TYPE: DNA
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Hypothetical sequence
155 <400> SEQUENCE: 11
156 tccccaaggc 10
158 <210> SEQ ID NO: 12
159 <211> LENGTH: 10
160 <212> TYPE: DNA
161 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: Hypothetical sequence
166 <400> SEQUENCE: 12
167 cccaaggcgc 10
169 <210> SEQ ID NO: 13
170 <211> LENGTH: 10
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Hypothetical sequence
177 <400> SEQUENCE: 13
178 cccaaggcgc 10
180 <210> SEQ ID NO: 14
181 <211> LENGTH: 10
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Hypothetical sequence
188 <400> SEQUENCE: 14
189 ccaaggcgca 10
191 <210> SEQ ID NO: 15
192 <211> LENGTH: 10
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: Hypothetical sequence
199 <400> SEQUENCE: 15
200 caaggcgcac 10
203 <210> SEQ ID NO: 16
204 <211> LENGTH: 30
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial sequence

RAW SEQUENCE LISTING

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Input Set : A:\35918.txt

Output Set: N:\CRF3\12062001\I479608A.raw

208 <220> FEATURE:
209 <223> OTHER INFORMATION: Hypothetical sequence
211 <400> SEQUENCE: 16
212 tgcttgccac aggtctcccc aaggcgact 30
215 <210> SEQ ID NO: 17
216 <211> LENGTH: 10
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: Hypothetical sequence
223 <400> SEQUENCE: 17
224 aggtctcccc 10
227 <210> SEQ ID NO: 18
228 <211> LENGTH: 10
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Hypothetical sequence
235 <400> SEQUENCE: 18
236 ggtctcccca 10
239 <210> SEQ ID NO: 19
240 <211> LENGTH: 10
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Hypothetical sequence
247 <400> SEQUENCE: 19
248 gtctcccaa 10
250 <210> SEQ ID NO: 20
251 <211> LENGTH: 10
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Hypothetical sequence
258 <400> SEQUENCE: 20
259 tctcccaag 10
261 <210> SEQ ID NO: 21
262 <211> LENGTH: 10
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Hypothetical sequence
269 <400> SEQUENCE: 21
270 ctccccaagg 10
272 <210> SEQ ID NO: 22
273 <211> LENGTH: 10
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:

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Input Set : A:\35918.txt
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278 <223> OTHER INFORMATION: Hypothetical sequence
280 <400> SEQUENCE: 22
281 tccccaaggc 10
283 <210> SEQ ID NO: 23
284 <211> LENGTH: 10
285 <212> TYPE: DNA
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Hypothetical sequence
291 <400> SEQUENCE: 23
292 ccccaaggcg 10
294 <210> SEQ ID NO: 24
295 <211> LENGTH: 10
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Hypothetical sequence
302 <400> SEQUENCE: 24
303 cccaaggcgc 10
305 <210> SEQ ID NO: 25
306 <211> LENGTH: 10
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial Sequences
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Hypothetical sequence
314 <400> SEQUENCE: 25
315 ccaaggcgca 10
317 <210> SEQ ID NO: 26
318 <211> LENGTH: 10
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: Hypothetical sequence
325 <400> SEQUENCE: 26
326 caaggcgcac 10
328 <210> SEQ ID NO: 27
329 <211> LENGTH: 10
330 <212> TYPE: DNA
331 <213> ORGANISM: Artificial Sequence
333 <220> FEATURE:
334 <223> OTHER INFORMATION: Hypothetical sequence
336 <400> SEQUENCE: 27
337 caggtctccc 10
339 <210> SEQ ID NO: 28
340 <211> LENGTH: 10
341 <212> TYPE: DNA
342 <213> ORGANISM: Artificial Sequences
344 <220> FEATURE:
345 <223> OTHER INFORMATION: Hypothetical sequence

VERIFICATION SUMMARY

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